

# Genetic diversity among Angus, American Brahman, Senepol and Romosinuano cattle breeds

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## Summary

The objective of this study was to quantify the genetic diversity among breeds under evaluation for tropical adaptability traits that affect the performance of beef cattle at the USDA/ARS SubTropical Agricultural Research Station (STARS) near Brooksville, FL, USA. Twenty-six microsatellite loci were used to estimate parameters of genetic diversity among the breeds American Brahman, Angus, Senepol and Romosinuano; the latter was comprised of two distinct bloodlines (Costa Rican and Venezuelan). Genotypes of 47 animals from each of these STARS herds were analysed for genetic diversity and genetic distance. Using two methods, the greatest genetic distance was detected between the Costa Rican line of Romosinuano and the Senepol. Gene diversity ranged between 0.64 (Costa Rican line of Romosinuano) and 0.75 (American Brahman). The breed relationship inferences, which are based on genetic distance, provide additional tools for consideration in future cross-breeding studies and for testing the relationship between quantified breed diversity and observed heterosis.

**Keywords** beef breeds, genetic distance, genetic variation, inbreeding, microsatellites, tropics.

## Introduction

Considerable interest and research has been generated in recent years regarding similarities and differences in cattle breeds from the perspective of potential genetic contributions to breeding programmes. Population geneticists explain taxonomic divergence and selection as an evolutionary process, which evolves from a pandemic into separate species and subspecies over several thousands to millions of years. With a parallel philosophy, today's modern breeds of domestic cattle have been developed from their wild ancestors. This was accomplished through natural selection in a plethora of ecosystems, accelerated by artificial trait selection pressure over the past few thousand years.

The USDA/ARS SubTropical Agricultural Research Station (STARS), Brooksville, FL, USA, evaluates tropical breeds of cattle that may harbour genetic potential to improve cattle breeding programmes in hot and humid climates. Because of declining numbers of adapted breeds in tropical regions of the world (Medrano 2000), a systematic method for rapid genetic evaluation of such diverse cattle breeds is needed. Rare breeds provide opportunities for increasing genetic diversity (Notter 1999) with respect to modern and extensively used cattle breeds in America. The objective of this study was to quantify the genetic diversity and genetic distance among the breeds used at STARS.

## Materials and methods

### Samples

The five breeding herds under evaluation are: (i) tropically adapted Angus (A), which were bred and selected out of the Wye Angus bloodline (Brinks & Katsigianis 1982); (ii) American Brahman (B), which were selected for production and meat quality traits (Vargas *et al.* 1999; Riley *et al.* 2002); (iii) descendants of Caribbean-imported (Butts 1988) Senepol (S); (iv) an upgraded herd of Costa Rican Romo-

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Accepted for publication 29 October 2006

sinuano (Rc); and (v) a purebred Venezuelan line of Romosinuano (Rv). The two Romosinuano lines were imported as embryos (Chase 1996). Forty-seven individuals were sampled from each population. The genotyping protocol (Brenneman *et al.* 2001) followed a 96-well microtitre plate format; thus, two sets of 47 individuals and positive and negative controls could be amplified simultaneously.

### Laboratory procedures

Whole blood was collected from live animals at STARS, and buffy coats were isolated. DNA was extracted from buffy coats or semen as applicable. Twenty-six microsatellite markers (Table S1) across 20 chromosomes were selected, amplified, visualized and scored as described in Brenneman *et al.* (2001).

### Data analysis

Multilocus genotypes were analysed using the GENEPOP v3.2a web-based platform (Raymond & Rousset 1995). The populations were analysed individually with exact Hardy–Weinberg tests (Guo & Thompson 1992) calculated across all loci to detect departures from Hardy–Weinberg equilibrium (HWE). Population uniqueness was detected by private allele frequencies. Excess homozygosity within populations ( $F_{IS}$ ) was estimated using methods by Weir & Cockerham (1984) and Robertson & Hill (1984). Wright's  $F_{ST}$  was estimated to quantify breed differentiation, both pairwise and among populations. Nei's (1972) standard ( $D_S$ ) and Nei *et al.*'s (1983) improved ( $D_A$ ) genetic distances were estimated using the GENEDIST genetic distance calculator.

## Results and discussion

Significant departure from HWE was detected for a single but different locus in all populations ( $P < 0.01$ ) except Brahman (B) following the Bonferroni correction for multiple tests. The uniqueness among populations was supported by a mean frequency for private alleles of 0.102. The average  $F_{ST}$  value of 0.238 indicates that nearly 24% of the genetic variation among these populations was due to breed differentiation. A total of 313 alleles (mean number of alleles = 12.0 per locus) was detected.

Marker data by breed type are reported in Table S1, and allele distributions in Fig. S1. Heterozygosity values, HWE, average alleles and allelic richness by breed type are reported in (Table 1). The private allele frequencies,  $F_{ST}$  values and genetic distances ( $D_S$  and  $D_A$ ) are ranked for each pairwise comparison of the five populations in Table S2. POPTREE was used to construct a phylogram (Takezaki & Nei 1996) based on  $D_A$  estimates to visualize the breed relationships (Fig. 1).

**Table 1** Genetic diversity data for five cattle breeds genotyped at 26 microsatellite loci.

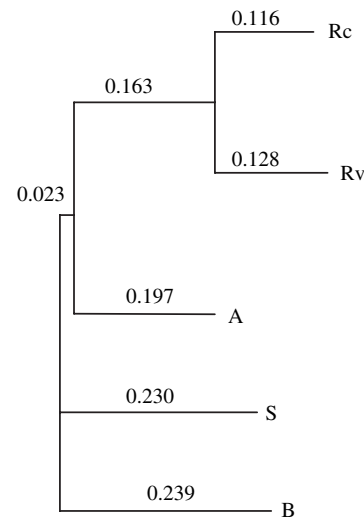
Population	Symbol	$k$ (SD) <sup>1</sup>	HWE <sup>2</sup>	AR (SD) <sup>3</sup>	$H$ (SD) <sup>4</sup>
Angus	A	5.5 (3.7)	25	5.3 (1.8)	0.66 (0.11)
Brahman	B	8.7 (6.8)	26	8.2 (2.3)	0.75 (0.11)
Senepol	S	6.6 (3.9)	25	6.3 (1.8)	0.69 (0.15)
Upgraded Romosinuano	Rc	5.6 (1.7)	25	5.0 (2.0)	0.64 (0.16)
Purebred Romosinuano	Rv	5.1 (4.6)	25	5.5 (1.2)	0.68 (0.13)

<sup>1</sup>Mean number of alleles.

<sup>2</sup>Number of loci in Hardy–Weinberg equilibrium (HWE) ( $P > 0.01$ ) after Bonferroni's correction for multiple tests.

<sup>3</sup>Allelic richness.

<sup>4</sup>Gene diversity.



**Figure 1** Phylogram of five cattle breeds [Angus (A), Brahman (B), Senepol (S), upgraded Romosinuano (Rc) and purebred Romosinuano (Rv)] using Nei *et al.*'s (1983) improved genetic distances ( $D_A$ ) as branch lengths.

Heterozygosities by breed (Table S1) were similar to those reported by Arranz *et al.* (1996) in Spanish cattle, Peelman *et al.* (1998) in Belgian cattle and Russell *et al.* (2000) in Mexican Criollo. The heterozygosities by locus were generally lower, while more alleles were detected than previously reported in the MARC (<http://www.marc.usda.gov/>) marker database (Fig. S1). As opposed to random mating, elevated  $F_{IS}$  should be expected in domestic livestock, given finite population sizes, selection for production traits and implementation of designed breeding programmes, which are all violations of HWE assumptions that can result in biased  $F_{IS}$  estimates. Two genetic distance parameters are presented as baselines for estimates of genetic differentiation. Takezaki & Nei (1996) investigated multiple methods for calculating genetic dis-

tance and suggested the application of the Nei *et al.* (1983) 'improved' genetic distance ( $D_A$ ) for microsatellite data. Nei's (1972) standard genetic distance ( $D_S$ ) is reported by convention.

Estimates of breed diversity might be useful to help rank little-studied but regionally successful breed candidates (Mateus *et al.* 2004) for the likelihood of integrating novel genetics into niche environments where many breed types are maladapted. These data should provide baseline values to initiate research on assessing relationships among well known and understudied breeds, as well as the application of genetic diversity and genetic distance parameters in livestock production. Genetic distance estimates may provide a means to quantify genetic diversity and thus determine if a relationship exists between genetic distance estimates and observed heterosis.

## Acknowledgements

Appreciation is extended to Dr C.N. Murphy (University of Missouri) and Dr A. Tewolde (CATIE) for their roles in providing the Rc bloodline; Drs J. Beltran, P. Bastidas and J. Troconiz (Universidad Central de Venezuela and ASOROMO) for their roles in providing the Rv bloodline; Dr J. L. Griffin (Reproductive Technology International) for providing expertise in embryo transfer and the STARS staff for providing technical assistance and animal care. The authors also thank Dr Max Mariasegaram for constructive suggestions in the final preparation of this paper.

Names are necessary to report factually on available data; however, the USDA neither guarantees nor warrants the standard of the product to the exclusion of others that may also be suitable.

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## Supplementary Material

The following supplementary material is available for this article online at <http://www.blackwell-synergy.com/doi/full/10.1111/j.1365-2052.2006.01551.x>

**Table S1** Chromosomal locations, number of alleles (observed and previously reported), heterozygosities by breed and locus (averaged and previously reported) and  $F_{ST}$  values for 26 microsatellite markers in all five populations.

**Table S2** Ranking of pairwise population comparisons for the population genetic parameters  $D_S$  (Nei's standard genetic distance),  $D_A$  (Nei's 'improved' genetic distance),  $F_{ST}$  (population substructure) and Pvt alleles (frequency of

alleles unique or private to either of the compared populations).

**Figure S1** Allele fragment sizes (in nucleotides) ( $x$ -axis) and allele frequencies ( $y$ -axis) observed for 26 microsatellite loci in five breed populations: Angus (A), American Brahman

(B), Senepol (S), purebred Romosinuano (Rv) and upgraded Romosinuano (Rc).

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